

CCACGGCTCCGGTCAGCTCTGGTTCGAGAAAGCAGCGGCTGGGCTGGGCTCCGGGGAATGGGC
 CCCCTCTGACCTAGTGTTCGGGGGCAAAAGGGTCTTCCCGGCTCGCTCGTGGAGGGGCTAT
 TTGGGCGCTGAGCGCGGCTGGAGGCTTGGAGCGCGCGCAGCAGGGGGCACACCGGGAACCG
 CCTGAGCGCGCGGACCATGACCGGGAGGGCTCTGCGCGCGGCTGGGACCATTTCTCTACCA
 CAACTCCCGACCTCGCTACCTGAGCGCGGGGCTTGGCACTGTGTCTCGCGCGCTGGCAGG
 CAGACTGGCGCTCCAGGTGGCGCTGAAGCAGCTGCACATCCCACTCCGCTCGTCCACAGTGAA
 AGAAGGATGTCTTACAGAACTGAAATTTTACACAAAGCTAGATTTAGTTACATTTCTTCAAT
 TTTGGGAATTTCAATGAGCGTCAATTTTGGGAATAGTTACTCAATACATGCGCAATGATCAT
 TAAATGAACCTCTACATAGGAAACTCAATATCTCTGATGTTGCTTGGCCATTGAGATTTCTTATC
 CTGCAATGAAATTTGGCTTGGTGTAAATTAAGTGCACAAATATGACTCCTCTTACTTCTCATGTA
 CTTGAAGACTCAGAATATCTTATGACAAATTTCTATGTTTAAAGATTCAGATTTTGGTTTAT
 CAAAGTGGCGCATGATGTCTCTCAGCTCAGCAAGTAGCAATCTGCACCAAGGAGGGGACA
 ATTATCTATATGCCACCTCAAAACTATGAACCTGGACAAAAATCAAGGGCCAGTATCAAGCACGA
 TATATATAGCTATGCACTTATCAGATGGGAAGTGTATCCAGAAAACAGCCTTTTGAAGATGTCA
 CCAATCCTTTGCGAGATAATGTATAGTGTGTCAAGGACATCCACCTGTTATTAATGAAGAAAGT
 TTGCCATATGATATACCTCAGCGAGCAGTATGATCTCTCTAATAGAAAGTGGATGGGCACAAAA
 TCCAGATGAAAGACCATCTTTCTTAAATGTTTATAGAACTTCAACCAAGTTTTCAGAACATTTG
 AAGAGATAACTTTCTTGAAGCTGTTATTCAGCTTAAAGAAAACAAAGTTACAGAGTGTTCAGT
 CCTTTCACCTATGTGACAGAGAGAAAAATGGAATTTCTCTCAACATACCTGTAATCATGGTCC
 ACAAGAGGAATCATGTGGATCTCTCAGCTCCATGAAAAATAGTGGTTCTCTGAAACTTCAAGGT
 CCTGCCAGCTCTCAAGACAAATGATTTTCTTATGAAAGCTCAAGACTGTTATTTTATGAAG
 CTGCATCACTGTCTGGAAATCAGAGTTGGGATAGCACCATTTCTGGATCTCAAGGGGCTGCATT
 CTGTGATCACAAGACCATTTCTTCTCTTCAAGCAATAATAATCCACTCTCAACTGCAGGAAACT
 CAGAACGTCTGCAGCTTGGTATAGCGGAGGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAAC
 CAAATGACAGAAGCCTGCTTACCAGTCTGCTAGATGCCCTTCTGTCCAGGGACTTGCATGAA
 AGAGGACTATGAACTTGTAGTACCAAGCCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACA
 CTACTGACATCCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATACAAACAA
 ATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTAAATTTACTTCA
 AAATAAAGCATGTAAAGTGAAGTGTCTTCAAGAAGAAATGTGTTTCAATAAAGGATATTTATAAA
 AA (SEQ ID NO:1)

FIG. 1

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Met	Asn	Gly	Glu	Ala	Ile	Cys	Ser	Ala	Leu	Pro	Thr	Ile	Pro	Tyr	His	Lys	Leu	Ala	Asp	10
Leu	Arg	Tyr	Leu	Ser	Arg	Gly	Ala	Ser	Gly	Thr	Val	Ser	Ser	Ala	Arg	His	Ala	Asp	Tyr	40
Arg	Val	Gln	Val	Ala	Val	Lys	His	Leu	His	Ile	His	Thr	Pro	Leu	Leu	Asp	Ser	Gln	Arg	60
Lys	Asp	Val	Leu	Arg	Glu	Ala	Glu	Ile	Leu	His	Lys	Ala	Arg	Phe	Ser	Tyr	Ile	Leu	Pro	80
Ile	Leu	Gly	Ile	Cys	Asn	Glu	Pro	Glu	Phe	Leu	Gly	Ile	Val	Thr	Glu	Tyr	Met	Pro	Asn	100
Gly	Ser	Leu	Asn	Glu	Leu	Leu	His	Arg	Lys	Thr	Glu	Tyr	Pro	Asp	Val	Ala	Trp	Pro	Leu	120
Arg	Phe	Arg	Ile	Leu	His	Glu	Ile	Ala	Leu	Gly	Val	Asn	Tyr	Leu	His	Asn	Met	Thr	Pro	140
Pro	Leu	Leu	His	His	Asp	Leu	Lys	Thr	Gln	Asn	Ile	Leu	Leu	Asp	Asn	Gln	Phe	His	Val	160
Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ser	Lys	Trp	Arg	Met	Met	Ser	Leu	Ser	Gln	Ser	Arg	Ser	180
Ser	Lys	Ser	Ala	Pro	Glu	Gly	Gly	Thr	Ile	Ile	Tyr	Met	Pro	Pro	Glu	Asn	Tyr	Gln	Pro	200
Gly	Gln	Lys	Ser	Arg	Ala	Ser	Ile	Lys	His	Asp	Ile	Tyr	Ser	Tyr	Ala	Val	Ile	Thr	Trp	220
Ile	Val	Leu	Ser	Arg	Lys	Gln	Pro	Phe	Glu	Asp	Val	Thr	Asn	Pro	Leu	Gln	Ile	Met	Tyr	240
Ser	Val	Ser	Gln	Gly	His	Arg	Pro	Val	Ile	Asn	Glu	Glu	Ser	Leu	Pro	Tyr	Asp	Ile	Pro	260
His	Arg	Ala	Arg	Met	Ile	Ser	Leu	Ile	Glu	Ser	Gly	Trp	Ala	Gln	Asn	Pro	Asp	Gln	Arg	280
Pro	Ser	Phe	Leu	Lys	Cys	Leu	Ile	Glu	Leu	Glu	Pro	Val	Leu	Arg	Thr	Phe	Glu	Gln	Ile	300
Thr	Phe	Leu	Glu	Ala	Val	Ile	Gln	Leu	Lys	Lys	Thr	Lys	Leu	Gln	Ser	Val	Ser	Ser	Ala	320
Ile	His	Leu	Cys	Asp	Lys	Lys	Lys	Met	Glu	Leu	Ser	Leu	Asn	Ile	Pro	Val	Asn	His	Gly	340
Pro	Gln	Glu	Glu	Ser	Cys	Gly	Ser	Ser	Gln	Leu	His	Glu	Asn	Ser	Gly	Ser	Pro	Glu	Thr	360
Ser	Arg	Ser	Leu	Pro	Ala	Pro	Gln	Asp	Asn	Asp	Phe	Leu	Ser	Arg	Lys	Ala	Gln	Asp	Cys	380
Tyr	Phe	Met	Lys	Leu	His	His	Cys	Pro	Gly	Asn	His	Ser	Trp	Asp	Ser	Thr	Ile	Ser	Gly	400
Ser	Gln	Arg	Ala	Ala	Phe	Cys	Asp	His	Lys	Thr	Ile	Pro	Cys	Ser	Ser	Ala	Ile	Ile	Asn	420
Pro	Leu	Ser	Thr	Ala	Gly	Asn	Ser	Glu	Arg	Leu	Gln	Pro	Gly	Ile	Ala	Gln	Gln	Trp	Ile	440
Gln	Ser	Lys	Arg	Glu	Asp	Ile	Val	Asn	Gln	Met	Thr	Glu	Ala	Cys	Leu	Asn	Gln	Ser	Leu	460
Asp	Ala	Leu	Leu	Ser	Arg	Asp	Leu	Ile	Met	Lys	Glu	Asp	Tyr	Glu	Leu	Val	Ser	Thr	Lys	480
Pro	Thr	Arg	Thr	Ser	Lys	Val	Arg	Gln	Leu	Leu	Asp	Thr	Thr	Asp	Ile	Gln	Gly	Glu	Glu	500
Phe	Ala	Lys	Val	Ile	Val	Gln	Lys	Leu	Lys	Asp	Asn	Lys	Gln	Met	Gly	Leu	Gln	Pro	Tyr	520
Pro	Glu	Ile	Leu	Val	Val	Ser	Arg	Ser	Pro	Ser	Leu	Asn	Leu	Leu	Gln	Asn	Lys	Ser	Met	540

(SEQ ID NO:2)

FIG. 2

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TTTTATGGG AATGCCAGCT TGGAGAGAG AGARCAATTC GAGAAWAAA TTTAAATTC
 AGATTACCC AATGTTCTTT TAAAATATTC TAACTTCAAA GAATGATGCC AGAAGCTTAA
 AAGGGGCTTC GCAGAGTAGC AGGGGGCTTT GAGGGGGGGG CCTGAATCCT GATTGGCTTT
 TTCTGAGAG GACACAGGCA GCTGAAGATG AATTTGGGA AAGTAGCCGC TTCTACTTT
 AACTATGGA GAGCAGGGCC AGAGTGAGAT GGAATATTC CCATCAGAGT CTCACCCCA
 CATTCAATTA CTGAAAAGCA ATCGGGAATC TTTGCTCACT CACATCCGCA ATACTCAGTG
 TCTGCTGAC AACTTCTCTA AGAATGACTA CTTCTCGGCC GAAGATGCCG AGATTCTGTG
 TCCCTCGCCC ACCCAGCCTC ACAAGGTCCC GAAATTTCTG GACCTGCTAC AGAGCAAGGG
 CGAGGAGGTG TCCGAGTTCT TCTCTACTTT GCTCCAGCAA CTGCGAGATG CCTACGTGCA
 CCTCAGGCTT TGGTCTCTGG AGATCGGCTT CTGCGCTTCC CTGCTCACTC AGAGCAAAGT
 CTGCTCAAC ACTGACCCAG TTAGCAGGTA TACCGAGCAG CTGCGACACC ATCTGGGCC
 TCACTCTAG TCTGCTCTCT GCTATGCCCA GAAGGAGGAG CTGCTCTCTG AGGAGATCTA
 CATGGACACC ATCATGGAGC TGGTTGGCTT CAGCAATGAG AGCCTGGGCA GCCTGAACAG
 CTTGGCCTGC CTCTGGAGC ACACCAAGCG CATCTCTAAT GAGCAGGGTG AGACCATCTT
 CATCTCTGGT GATGCTGGGG TGGCAAGTC CATGCTGCTA CAGCGGCTGC AGAGCCTCTG
 GGCACCGGGC CGGCTAGAGC CAGGGGTCAA ATTCTTCTTC CACTTTGCTT GCGGCATGTT
 CAGCTCTTTC AAGGAAAGTG ACAGGCTCTG TCTGCAGGAC CTGCTCTTCA AGCACTACTG
 CTACCCAGAG CGGGACCCCG AGGAGGTGTT TGGCTTCTG CTGCGCTTCC GGCAGCTGGC
 CTTCTTCAAC TTGATGGCC TGGACGAGCT GCACTCGGAC TTGGACCTCA GCGCGCTGCC
 TACAGCTCC TGGCCTGGG AGCCTGCGCA GCGCCTGCTC TTGCTGGCCA ACCTGCTCAG
 TGGAAAGCTG CTGAAGGGGG CTAGCAAGCT GCTCAGAGCC GGCACAGGCA TGGAGGTGCC
 GCGCCAGTTC CTGCGGAAGA AGGTGCTTCT CCGGGGCTTC TCCCGCAGCC ACCTGCGGCG
 CTATGCCAGG AGGATGTTCC CCGAGCGGCG CTTGCAGGAC CGCCTGCTCA GGCAGCTGGA
 GGCACACCCC AACCTCTGCA GCCTGTGCTC TGTGCCCCCTC TTCTGCTGGA TCATCTTCCG
 GTGCTTCCAG CACTTCCCTG CTGCTTTTCA AGGCTCACCA CAGCTGCCCC ACTGACCAT
 GACCTGACA GATGTTCTTC TCTGCTCAC TTAGGTCCAT CTGAACAGGA TGCAGCCGAG
 CAGCCTGCTG CAGCGGAACA CACCGAGCCC AGTGGAGACC CTCCAGCCCG GCGGGGACAC
 TCTGCTCTCG CTGGGGCAGG TGGCCACCG GGGCATGGAG AAGAGCCTCT TTGCTTTCAC
 CAGGAGGAG GTGCAGGCTT CCGGGCTGCA GGAGAGAGAC ATGCAGCTGG GCTTCTCTCG
 GGTCTTCCCG GAGCTGGGCC CCGGGGTGA CAGCAGTCC TATGAGTTTT TGCACCTCAG
 CTTGAGGCC TTCTTACAG CTTCTTCTCT GCTGCTGGAC GACAGGGTGG GCACTCAGGA
 CTTCTCAGG TTCTTCCAGG AGTGGATGCC CCGTGGGGGG GCAGCGACCA CTTCTCTCTA

FIG. 3 (page 1 of 2)

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TCTTCGCTTC CTCCGCTTCC AGTGGCTGCA GGGCAGTGGT CCGCGCGCGG AAGACCTCTT
 TAAGAACAAG GATCACTTCC AGTTACCAAA CCTCTTCTTC TCGGGGCTGT TGTCCAAAGC
 TAAACAGAAA CTCTTCCGCG ATCTGCTGCC CCGCGCAGCC CTCAGGAGAA AGCGCAAGGC
 TCTGTGGGCA CACCTGTTTT CCAAGCTGCG GGGCTACCTG AAGAGCCTTC CCGCGCTTCA
 TGTGAAAGC TTCAACCAAG TCAAGGCGAT CCGCAGCTTC ATCTGGATGC TCGGCTGCAT
 TTACGAGACA CAGAGCCAGA AGGTGGGGCA GCTGGCGCGC AGGGGCTCTT GCGCCAACTA
 TCTCAAGCTG ACCTACTGCA ACCTCTCTTC GCGCGACTTC AGCGCGCTCT CTTTCTCTCT
 GCATCACTTC CCGAAGCGGC TCGCCCTAGA CCTAGACAAC AACATCTCA ACGACTACGG
 CCGTGGGGAG CTGCAGCCCT GCTTCAGCGG CCTCACTGTT CTCAGACTCA GCGTAAACCA
 GATCACTGAC GGTGGGGTAA AGGTGCTAAG CCAAGAGCTG ACCAAATACA AAATTGTGAC
 CTATTTGGGT TTATACAACA ACCAGATCAC CCAATCTGGA GCGAGGTACG TCACCAAAAT
 TCTGGATGAA TCAAAAGGCC TCAAGCATCT TAACTGGA AAAACAAAA TAACAAGTCA
 AGGAGGGAAG TATCTGCGCC TCGCTGTGAA GAACAGCAAA TCAATCTCTG AGGTGGGAT
 GTGGGGCAAT CAAGTTGGGG ATGAAGGAGC AAAAGCCTTC GCAGAGGCTC TCGGGAACCA
 CCCCAGCTTC ACCACCCCTCA GTCTTCTCTC CAACGGCATC TCCACAGAAG GAGGAAAGAG
 CCTTGGGAGG GCGCTGCAGC AGAACAGCTC TCTAGAAATA CTGTGGCTCA CCGAAATCA
 ACTCAACGAT CAAGTGGCAG AGAGTTTGGC AGAAATGTTG AAAGTCAACC AGACGTTAAA
 GCATTTATGG CTTATCCAGA ATCAGATCAC AGCTAAGGGG ACTGCCCCAGC TCGCAGATGC
 GTTACAGAGC AACACTGGCA TAACAGAGAT TTGCTTAAAT GGAACCTCA TAAACCAGA
 TGAGGCCAAA GTCTATGAAG ATGAGAAGCG GATTATCTCT TTCTGAGAGG ATGCTTTCTT
 TTCTATGGGG TTTTGGCCCT CGAGCCTGAG CAGCAATGC CACTCTGGGC AGTCTTTTCT
 TCAAGTGTCT TAAAGGGGCG TCGCGAGCGG GCACTATCAG GAGTCCACTG CCTTCATGAT
 GCAAGCCAGC TTCTGTGCA GAAGGTCTCG TCGGCAAACT CCTAAGTAC CCGCTACAAT
 TCTGCAGAAA AAGAATGTGT CTTGCGAGCT GTTGTAGTTA CAGTAAATAC ACTGTGAAGA
 GAAAAAAAA ACGGACGCGT GG (SEQ ID NO:7)

FIG. 3 (page 2 of 2)

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WEEQCHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIWCACFTQP
CKVRKILLVQSKGZEVSEFFLYLLQQLADAYVDLRFWLLLEIGFSPSLLTQSKVVVNTDFVSRYT
QQLRHHLCGRDSKFVLCYAKKEELLLEETVMDTIMELVGFSNESLGSLNSLACLDDHTTGTILNEQG
ETIFELGDAGVGKSMILLQRLQSLNATGRLEAGVKFFTHFRCRMFSCTKESDRLCLQDLLFKHYCY
PERDPHEVFAFLLRFPHVALFTFDGLDELHSDLDLSRVPDSSCFWEPAPHLVLLANLLSGKLLKG
ASKELTARTGIEVPRQFLAKXVLLAGFSPSHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSV
PLFCNIIIFRCFQHFRAAFEGSFQLPDCTMTLTDVLLVTEVHLNRMQPSSLVQRNTRSPVETLHA
GRDTLCSLGQVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFLRALPELGFGGDQQSYEFFHLTL
QAFFTAFFLVLDDEVGTQELLRFQEWMPFAGAATTSCYPPFLPFQCLQGSGPAREDLFKNKDH
QFTNLFLCGLLSKAKQKLEHLVFAAALRRKRKALNAHLFSSLRGYLKSLPRVQVESFNQVQAMP
TFIWMLRCTIYETQSQKVGQLAARGICANYLKLTYCNACSDCSALSFVLHHFPKRLALDLENNNL
NDYGVRELQPCFSRLTVLRLSVNQITDGGVKVLSEELTKYKIVTYLGLYNNQITDVGARYVTKIL
DECKGLTHLKLGNKITSEGGKYLALAVKNSKSISEVGMWGNQVGDEGAKAFEAALANHPSLTTL
SLASNGISTEGGKSLARALQQNTSLEILNLTCNELNDEVAESLAEMLKVNQTLKHLWLIQNQITA
KGTAQLADALQSNTGITEICLNGNLINPFEAKVYEDEKRIICF (SEQ ID NO:8)

FIG. 4

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TACGGCTCCSACTTCTGAGAAATGACTACTTCTCGGCCAAGATGCGGAGATTSTGT
TTGCCCTSCCCCAACCAGCCTGACAGGTCCSCAAAATTCTGGACCTGGTACAGAGCAAG
TGGGAGGAGGTGTCCGAGTTCTTCTCTACTTCTCTCAGCACTCCAGATGCCCTACGT
TGACCTCAGGCCCTTSGGCTGCTGAGATCGGCTTCTCCCTTCCCTCACTCAGAGCA
AAGTCTGGTCAACACTGACCCAGTGAGCAGGTATACCCAGCAGCTGCGACACCATCTG
TGGCTGACTGCAAGTTCTGCTGCTGCTATGCCCAAGAGGAGGAGCTGCTGCTGAGGA
EATCTACATGGACACCATCATGGAGCTGGTTGGCTTCAGCAATGAGAGCCTGGGCAGCC
TGAACAGCCTGGCCTGCCCTCCTGACCCACACCACCGGCATCCTCAATGAGCAGGGTGAG
ACCATCTTCATCCTGGGTGATGCTGGGTGGGCAAGTCCATGCTGCTACAGCGGCTGCA
TAGCCTCTGGGCCACGGGCCGGCTAGACGCGAGGGGTCAATTCTTCTTCCACTTTCGCT
TCCGCATGTTTCAGCTGCTTCAAGGAAAGTGACAGGCTGTGTCTGAGGACCTGCTCTTC
AAGCACTACTGCTACCCAGAGCGGGACCCCGAGGAGGTGTTTGCCTTCTGCTGCGCTT
CCCCCAGCTGGCCCTCTTCACTTTCGATGGCCTGGACGAGCTGCACTCGGACTTGGACC
TGAGCCCGCTGCTGACAGCTCTTGGCCCTGGGAGCCTGCCACCCCTGGTCTTGTCTG
GCCAACCTGCTCAGTGGGAAGCTGCTCAAGGGGGCTAGCAAGCTGCTCACAGCCCGCAC
AGGCATCGAGGTCCCGCGCCAGTTCTGCGGAAGAAGGTGCTTCTCCGGGGCTTCTCCC
TCAGCCACCTGCGCGCCTATGCCAGGAGGATGTTCCCGGAGCGGGCCCTGCAGGACCCG
TTGCTGAGCCAGCTGGAGGCCAACCCCAACCTCTGCAGCCTGTGCTCTGTGCCCTCTT
TTGCTGGATCATCTTCCGGTGTCTCCAGCACTTCCGTGCTGCCCTTTGAAGGCTCACAC
AGCTGCCCSACTGCACGATGACCCCTGACAGATGTCTTCTCTGGTCACTGAGGTCCAT
CTGAACAGGATGCAGCCCAGCAGCCTSGTGACGCGGAACACACGACGCCCAGTGGAGAC
CTTCCACGCGCGCGGACACTCTGTGCTGCTGGGGCAGGTGGCCACCGGGGCATGG
AGAAGAGCCTCTTTGTCTTCAACAGGAGGAGGTGCAGGCCCTCCGGCTGCAGGAGAGA
GACATGCAGCTGGGCTTCTTCCGGGCTTTGCCGGAGCTGGGCCCCGGGGGTGACCAGCA
GTCCTATGAGTTTTTCCACCTCAGCCTCCTCACCTGTAAAACTGGGATCCAGTATAGA
CTTTGGAATCAGTAGACACCATATGCTTCAAAAAACAGGGGCTATTAAAAATGACATCA
GGAGCCAGAAAGTCTCATGGCTGTGCTTTCTCTTGAAGTTTATACAACAACAGATCAC
CGATGTCCGAGCCAGACTGGGAAAAAACAAATAACAAGTGAAGGAGGGAAGTATCTCG
CCCTGGCTGTGAAGAACAGCAAATCAATCTCTGAGGTTGGGATGTGGGGCAATCAAGTT
GGGGATGAAGGAGCAAAGCCTTCCAGAGGCTCTGCGGAACCACCCCAGCTTGACCAC
CCTGAGTCTTGCGTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCTTGGGAGGGCCC
TGCAGCAGAACACGTCTCTAGAAATACTGTGGCTGACCCAAAATGAAGTCAACGATGAA
TTGGCAGAGAGTTTGGCAGAAATGTTCAAGTCAACCAGACGTTAAAGCATTTATGGCT
TATCCAGAAATCAGATCACAGTCTTTTGTGTGAGTGTCTTAAAGGGGCTTCCGAGGGCGG
GACTATCAGGAGTCCACTGCCCTCATGATGCAAGCCAGCTTCTGTGCAGAAAGTCTGG
TCGGCAAACTCCCTAAGTACCCGCTACAATTCTGCAGAAAAAGAATGTGTCTTGGCAGC
TGTGTAGTTACAGTAAATACACTGTGAAGAGACTTTATTGCCTATTATAATTATTTT
ATCTGAAGCTAGAGGAATAAAGCTGTGAGCAAAACAGAGGAGGCCAGCCTCACCTCATT
CAACACCTGCCATAGGGACCAACGGGAGCGAGTTGGTCACCGCTCTTTTCATTGAAGAG
TTGAGGATGTGGCACAAGTTGGTGCCAAAGCTTCTTGAATAAAACGTGTTTGTATGGATT
AGTATTATACCTGAAATATTTTCTTCTTCTCAGCACTTTCCCATGTATTGATCTGGT
CCCACTTCACAGCTGGAGACACCGAGTATGTGCAGTGTGGGATTTGACTCCTCCAAGG
TTTTGTGGAAAGTTAATGTCAAGGAAAGGATGCACCACGGGCTTTTAATTTTAATCCTG
GAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAGCTCTTAGCTGGTCTAAGA
ATGACGATGCCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTCCTCTGCTAGGCTACCT
CCTCTAGAAGGCTGAGTACCATGGGCTACAGTGTCTGGCCTTGGGAAGAAGTGATTCTG
TCCCTCCAAAGAAATAGGGCATGGCTTGGCCCTGTGGCCCTGGCATCCAAATGGCTGCT
TTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTTCTCTGCTGCCCTCCCAAGCAGCTGAAG
GGTGAATAAACGGGGCGCAAGACTCAGGGGATCGGCTGGGAAGTGGGCCAGCAGAGCAT
TTTGGACACCCCCCACCATGGTGGGCTTGTGGTGGCTCTCCATGAGGGTGGGGGTGAT
ACTACTAGATCACTTGTCTCTTGGCAGCTCATTTGTTAATAAAATACTGAAACACAA
AA
AAAAAAAAAAAA (SEQ ID NO:25)

FIG. 5

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HASDLLKNDYFSAEDAEIWCACFTQPKVRKILLVQSKGEEVSEFFLYLL
QQLADAYVDLRPWLLLEIGFSPSLLTQSKVWNTDPVSRYTQQLRHHLGRDS
KFVLCYAOKEELLLEETIMDTIMELVGFSNESLGSLSLACLLDHTTGILN
EQGETIFILGDAGVGKSMILLCRLQSLWATGRLDAGVKFFHFRCRMFSCFK
ESDRCLQDILLFKHYCYPERDPFEEVFAFLLRFPFHVALETFDGLDELHSDLD
LSRVPDSSCPWEPAPPLVLLANLLSGKLLKGASKLLTARTGIEVPROFLRK
KVLLRGFSPSHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSVPLFCWI
IFRCFQHFRAAFEGSPQLPDCITLTDVFLLVTEVHLNRMQPSSSLVQRNTR
SPVETLHAGRDTLCSLGQVAHRCMEKSLFVFTQEEVQASGLQERDMQLGFL
RALPELGPGGDQQSYEFFHLSLLTCKTGIFV (SEQ ID NO:26)

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FIG. 6

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	10	20	30	40	
1	EEHGH	LLKX	THIRNTQ	NDY	CARD1-CARD
2	QGGIAC	WQKEDIN	EA	SRDL	CARD3-CARD
3	ACSR	PSETDRE	KRL	ADSG	ARC-CARD
4	KACDE	SLLK	M	F	CARD1-CARD
5	KESNDIL	LLK	MALF	HL	CARD2-CARD

	50	60	70	80		
15	FSALDA	CECE	QDKE	KILLL	SEEVSEFFYL	CARD4-CARD
19	IMEDY	LLST	RTSK	QUL	ITDIQ	CARD3-CARD
27	LTGPEY	ALD	LDERR	RLILL	GC	ARC-CARD
35	YH	QED	I	QITQ	IL	CARD1-CARD
36	ITEQ	EDVI	Q	TQTS	LA	CARD2-CARD

	90	100		
75	EQLEDEYVDI	REW	EIGF	CARD4-CARD
79	EKDNKQ	MG	QPEI	CARD3-CARD
77	ARTG	POPAWDNQ	VG	ARC-CARD
75	EKEIDSTI	KN	F	CARD1-CARD
76	MAEAVI	EHL	F	CARD2-CARD

007027 120400

FIG. 7

00720721-120400

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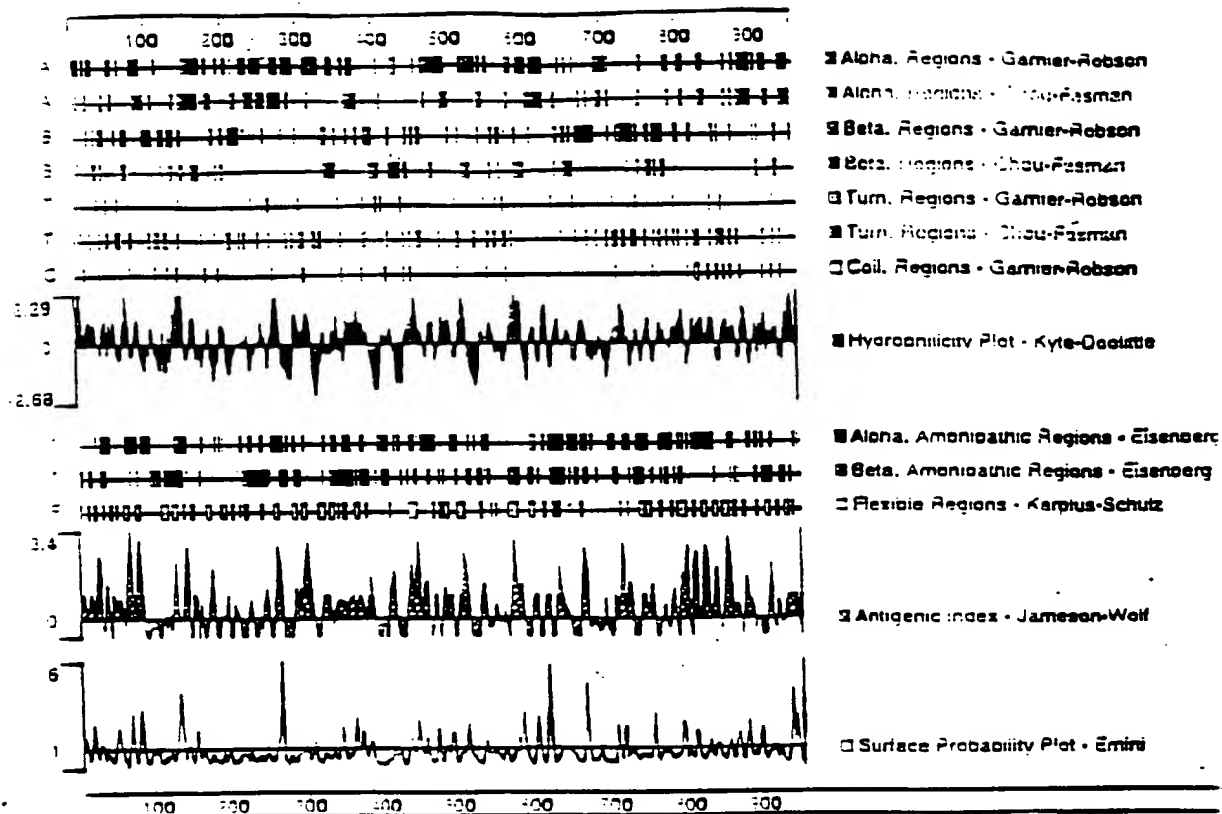


FIG. 8

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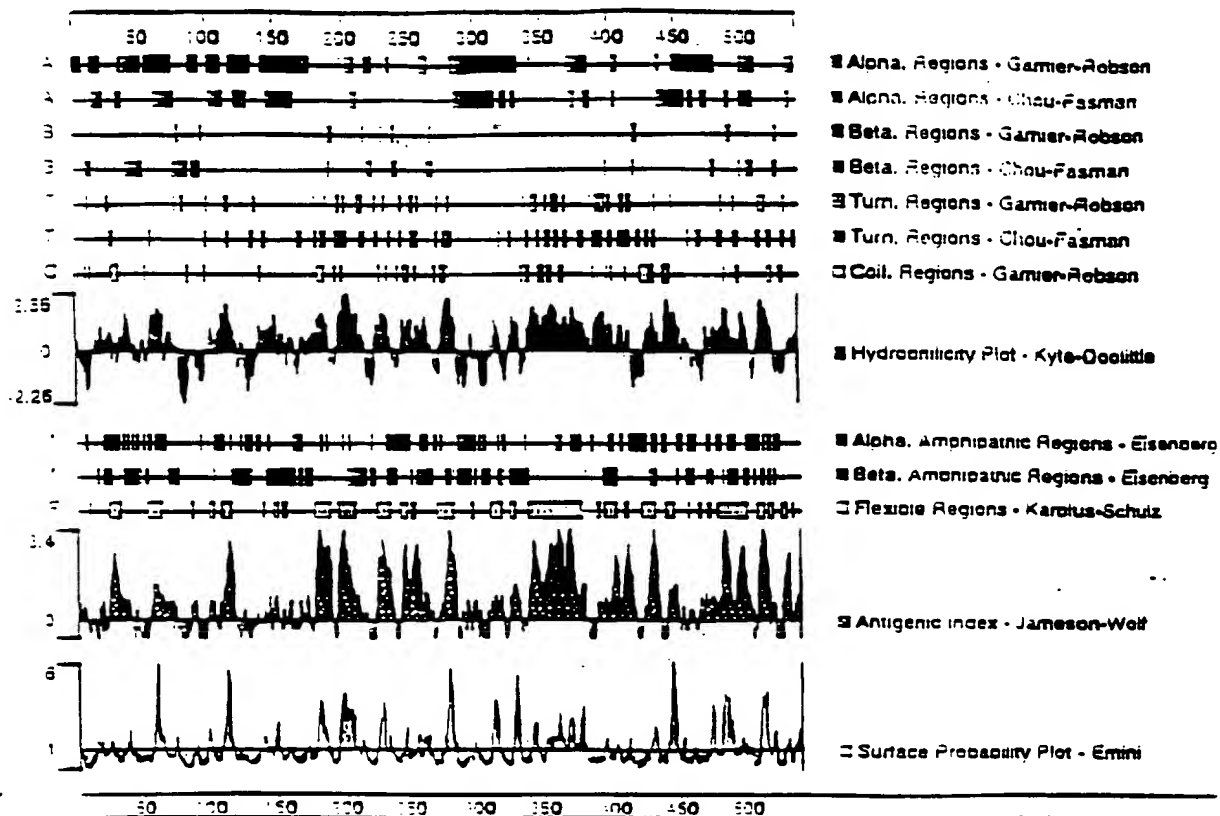


FIG. 9

[illegible]

FIG. 10 (Page 1 of 3)

007224-120100

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CCAGGGCCTTCTTTACAGCCTTCTTCTCTGCTGGACGACAGGGTGGGCACTCAGGAGCT
GCTCAGGTTCTTCCAGGAGTGGATGCCCCCTGCGGGGGCAGCGACCACTCTCTATCC
TCCCTTCTTCCCGTTCCAGTGCCTGCAGGGCAGTGGTCCCGCGCGGAAGACCTCTTCAA
GAACAAGGATCACTTCCAGTTCAACCAACCTCTTCTGTGCGGGCTGTTGKCCAAAGCCAA
ACAGAAACTCTGCGGCATCTGGTGCCCGCGGCAGCCCTGAGGAGAAAGCGCAAGGCCCT
GTGGGCACACCTGTTTTCCAGCCTGCGGGGCTACCTGAAGAGCCTGCCCCGCGTTCAAGT
CGAAAGCTTCAACCAGGTGCAGGCCATGCCACGTTTCTGATGCTGCGCTGCATCTA
CGAGACACAGAGCCAGAAGGTGGGGCAGCTGGCGGCCAGGGGCATCTGCGCCAACCTACCT
CAAGCTGACCTACTGCAACGCCTGCTCGGCCGACTGCAGCGCCCTCTCTCTCTCTGCA
TCACTTCCCCAAGCGGCTGGCCCTAGACCTAGACAACAACAATCTCAACGACTACGGCGT
GCGGGAGCTGCAGCCCTGCTTCAGCCGCTCACTGTTCTCAGACTCAGCGTAAACCAGAT
CACTGACGGTGGGGTAAAGGTGCTAAGCGAAGAGCTGACCAAATACAAAATTGTGACCTA
TTTGGGTTTATACAACAACCAGATCACCGATGTGCGAGCCAGGTACGTCAACCAAATCCT
GGATGAATGCAAAGGCCTCAGCATCTTAACTGGGAAAAAACAAAATAACAGTGAAGG
AGGGAAGTATCTCGCCCTGGCTGTGAAGAACAGCAAATCAATCTCTGAGGTGGGATGTG
GGGCAATCAAGTTGGGGATGAAGGAGCAAAAGCCTTCGAGAGGCTCTGCGGAACCAACC
CAGCTTGACCACCCTGAGTCTTGGCTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCT
TGCGAGGGCCCTGCAGCAGAACACGTCTCTAGAAATACTGTGGCTGACCCAAAATGAACT
CAACGATGAAGTGGCAGAGAGTTTGGCAGAAATGTTGAAAGTCAACCAGACGTTAAAGCA
TTTATGGCTTATCCAGAATCASATCACAGCTWARGGACTGCCCAGCTGGCAGATGCGTT
ACAGAGCAACACTGGCATAACAGAGATTTGCCTAAATGGAAACCTGATAAAACCAGAGGA
GGCCAAAGTCTATGAAGATCAGAAGCGGATTATCTGTTTCTGAGAGGATGCTTCTCTGTT
CATGGGGTTTTTGGCCCTGGAGCCTCAGCAGCAAATGCCACTYTGGGCAGTCTTTTGTGTC
AGTGTCTTAAAGGGGCCTGCGCAGGCGGGACTATCAGGAGTCCACTGGCTCCATGATGCA
AGCCAGCTTCTCTGTGCAGAAGGTCTGGTGGGCAAACTCCCTAAGTACCCGCTACAATTCT
GCAGAAAAAGAATGTGTCTTGGCAGCTGTTGTAGTTACAGTAAATACACTGTGAAGAGAC
TTTATTGCCTATTATAATTATTTTTATCTGAAGCTAGAGGAATAAAGCTGTGAGCAAACA
GAGGAGGCCAGCCTCACCTCATTCCAACACCTGCCATAGGGACCAACGGGAGCGAGTTGG
TCACCGCTCTTTTTATTGAAGAGTTGAGGATGTGGCACAAGTTGGTGCCAAGCTTCTTG
AATAAAACGTGTTTGATGGATTAGTATTATACCTGAAATATTTTCTTCTCTCAGCACT
TTCCCATGTATTGATACTGGTCCCCTTCAACAGCTGGAGACACCGGAGTATGTGCAGTGT
GGGATTGACTCCTCCAAGGTTTTGTGGAAAGTTAATGTCAAGGAAAGGATGCACCACGG

GCTTTTAATTTTAATCCTGGAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAG
CTCTTAGCTGGTCTAAGAATGACGATGCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTC
CTCTGCTAGGCTACCCCTCCTCTAGAAGGCTGAGTACCATGGGCTACAGTGTCTGGCCTTG
GGAAGAAGTGATTCTGTCCCTCCAAAGAAATAGGGCATGGCTTGCCCCCTGTGGCCCTGGC
ATCCAAATGGCTGCTTTTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTCTTCCTGCCTC
CCAAGCAGCTGAAGGGTGACTAAACGGGCGCCAAGACTCAGGGGATCGGCTGGGAACTGG
GCCAGCAGAGCATGTTGGACACCCCCCACCATGGTGGGCTTGTGGTGGCTGCTCCATGAG
GGTGGGGGTGATACTACTAGATCACTTGTCTCTTGCCAGCTCATTTGTTAATAAAATAC
TGAAAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGG (SEQ ID NO:38)

FIG. 10 (Page 3 of 3)

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MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCA
CPTQPKVRKILDLVQSKGEEVSEFFLYLLQQLADAYVDLRFWLLEIGFSPSLLTQSKV
VNTDPVSRYTQQLRHHLGKDSKFVLCYAKKEELLLEEIYMDTIMELVGFSNESLGSLNSL
ACLLDHTTGILNEQAASRKVTGCVCRSCSSSTTATQSGTFRRCCLPSCCASPTWPSSPSMA
WTSCRTIWT (SEQ ID NO:39)

FIG. 11

007287.1.120400

CACGCGTCCGCGCTACTCGGGAGCAGCGTCTCCCGGGCCACGGCGCTTCCCGGCCCCG
 GCGTCCCGGGACCATGGCGCTCTCCGGGCTCTTCTCTAGCTCTCAGCGGCTCGGAAGTCT
 GTAAACCTGGTGGCCAAGTGATTSTAGTCAGGAGACTTTCCTTCGGTTTCTGCCTTTGA
 TGGCAAGAGGTGGAGATTSTGGCGGCGATTACAGAAAACATCTGGGAAGACAAGTTGCTG
 TTTTATGGGAATCGCAGGCTTGGGAAGAGACAGAAGCAATTCCAGAAATAAATTGGAAAT
 TGAAGATTTAAACAATGTTGTTTTTAAATATTCTAACTTCAAAGAATGATGCCAGAACT
 TAAAAAGGGGCTGCGCAGAGTAGCAGGGGCCCCCTGAGGGGCGGGCCCTGAATCCTGATTGC
 CCTTCTGCTGAGAGGACACACGCAGCTGAAGATGAATTTGGGAAAAGTAGCCGCTTGCTA
 CTTTAACTATGGAAGAGCAGGGGCCACAGTGAGATGGAAATAATCCCATCAGAGTCTCACC
 CCCACATTCAATTACTGAAAAGCAATCGGGAACCTTCTGGTCACTCACATCCGCAATACTC
 AGTGTCTGGTGGACAACCTTGTCTGAAGAATGACTACTTCTCGGCCGAAGATGCGGAGATTG
 TGTGTGCTGCCCCACCCAGCCTGACAAGGTCCGCAAAATTCTGGACCTGGTACAGAGCA
 AGGGCGAGGAGGTGTCCGAGTTCTTCTCTACTTGCTCCAGCAACTCCAGATGCCTACG
 TGGACCTCAGGCCTTGGCTGCTGGAGATCGGCTTCTCCCCCTTCCCTGCTCACTCAGAGCA
 AAGTCGTGGTCAACACTGACCCAGGTAGGAGTCAGCCCCAGCAAGACCGCAGGCACCAAGT
 GCAAGCAGGGGCCCTGGGGGGTTTGGTAATGGCTGGGCCAGCCCTGAGTGCCACCTCAGGA
 AGCAGGGCCCAGGTGCTATTTTGATTTTAGAAAGGAACAGCTGAATCCTGTCTCCCAAGTG
 CAGCCCAGGTGGCTGCGATTGAACTGCCCACACCTCGATGGTCTGGTTTATAGAGGGGCC
 TTTGGAAGTATGGGAATGGCCTGTGTTCTGACCCCTTGCTTTCTTCTTCTGACATAT
 GTAGACATTTTAATGGTTGCACAAATTCAAGGTTGTATTTTTTTTTCTTTAAAAAATCT
 TTAGCTGGACATGGTAGCACACACCTGTAGTTCCAGCTACTCAGGAGGCTGAGGCAAGAG
 TACTGCTTGAGCCCCAGAGTCTAAGGCTGCAGCGAGCTATGATTGTGCCCCCTACACTCCA
 CAGCCTGGGTTTTAGAGTGAGACCCTGTCTCTAAAAA
 AAAAAAAAAAANGGGCGG (SEQ ID NO:40)

FIG. 12

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MEEQGHSEMEIIPSESHPHIQLLXSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCA
CPTQPDKVRKILDLVQSKGEZVSEFFLYLLQQLADAYVDLRFWLLEIGFSPSLLTQSKVV
VNTDFGRSQFQQDRRHQCKQGFGGSGNGWASPECHLRKQAQVLF
(SEQ ID NO:41)

FIG. 13

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00720724 120400

	MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCL	Majority
	10 20 30 40	
1	MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCL	CARD4-Y CLONE
1	MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCL	CARD4-Z CLONE
1	MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCL	CARD4L
	VDNLLKNDYFSAEDAEIVCACPTQPKVRKILDLVOSKGE	Majority
	50 60 70 80	
1	VDNLLKNDYFSAEDAEIVCACPTQPKVRKILDLVOSKGE	CARD4-Y CLONE
1	VDNLLKNDYFSAEDAEIVCACPTQPKVRKILDLVOSKGE	CARD4-Z CLONE
1	VDNLLKNDYFSAEDAEIVCACPTQPKVRKILDLVOSKGE	CARD4L
	EVSEFFLYLLOQLADAYVDLRPWLLLEIGFSPSLLTOSKVV	Majority
	90 100 110 120	
1	EVSEFFLYLLOQLADAYVDLRPWLLLEIGFSPSLLTOSKVV	CARD4-Y CLONE
1	EVSEFFLYLLOQLADAYVDLRPWLLLEIGFSPSLLTOSKVV	CARD4-Z CLONE
1	EVSEFFLYLLOQLADAYVDLRPWLLLEIGFSPSLLTOSKVV	CARD4L
	VNTDPVSRYTQOLRHHLGRDSKFVLCYAOKEELLLEEIYM	Majority
	130 140 150 160	
121	VNTDPVSRYTQOLRHHLGRDSKFVLCYAOKEELLLEEIYM	CARD4-Y CLONE
121	VNTDPGRSOPQQDRRI	CARD4-Z CLONE
121	VNTDPVSRYTQOLRHHLGRDSKFVLCYAOKEELLLEEIYM	CARD4L
	DTIMELVGFSNESLGSLSLACLDDHTTGILNEOXXXX -	Majority
	170 180 190 200	
161	DTIMELVGFSNESLGSLSLACLDDHTTGILNEOAAASR -	CARD4-Y CLONE
137	-----	CARD4-Z CLONE
161	DTIMELVGFSNESLGSLSLACLDDHTTGILNEOGETIFI	CARD4L
	-----XCXXXX	Majority
	210 220 230 240	
139	-----FVTVG	CARD4-Y CLONE
137	-----QCEQ	CARD4-Z CLONE
131	LG DAGVGKSM L L QRLQSLWATGR LDAGVKFFHFRCGRMFS	CARD4L
	-----XC-----	Majority
	250 260 270 280	
133	G-----V	CARD4-Y CLONE
141	-----	CARD4-Z CLONE
141	GFKESDRLGLQD L L FKH YCYPERDP EEFVFAFLLRFP HVAL	CARD4L
	-----KXCKXX-----	Majority
	290 300 310 320	
136	-----RTGSSS-----	CARD4-Y CLONE
141	-----	CARD4-Z CLONE
131	FTFDGLDELHSDLDLSRVDDSSGPWEPAPHPVLLANLLSG	CARD4L

FIGURE 14 (1 of 4)

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		-----TXXTXXXXP-----		Majority
		330 340 350 360		
122	-----	-----T T A T Q S S T P R-----		CARD4-Y CLONE
141	-----	-----T T A T Q S S T P R-----		CARD4-Z CLONE
161	-----	-----T T A T Q S S T P R-----		CARD4L
		-----R C-----		Majority
		370 380 390 400		
122	-----	-----R C-----		CARD4-Y CLONE
141	-----	-----R C-----		CARD4-Z CLONE
161	-----	-----R C-----		CARD4L
		-----L P X C-----		Majority
		410 420 430 440		
124	-----	-----L P S C-----		CARD4-Y CLONE
141	-----	-----L P S C-----		CARD4-Z CLONE
401	-----	-----L P S C-----		CARD4L
		-----Majority-----		
		450 460 470 480		
128	-----	-----Majority-----		CARD4-Y CLONE
141	-----	-----Majority-----		CARD4-Z CLONE
441	-----	-----Majority-----		CARD4L
		-----G P G G-----		Majority
		490 500 510 520		
128	-----	-----G P G G-----		CARD4-Y CLONE
141	-----	-----G P G G-----		CARD4-Z CLONE
481	-----	-----G P G G-----		CARD4L
		-----TXXTXXXXP-----		Majority
		530 540 550 560		
128	-----	-----TXXTXXXXP-----		CARD4-Y CLONE
145	-----	-----TXXTXXXXP-----		CARD4-Z CLONE
551	-----	-----TXXTXXXXP-----		CARD4L
		-----Majority-----		
		570 580 590 600		
131	-----	-----Majority-----		CARD4-Y CLONE
153	-----	-----Majority-----		CARD4-Z CLONE
561	-----	-----Majority-----		CARD4L
		-----TXX-----		Majority
		610 620 630 640		
132	-----	-----TXX-----		CARD4-Y CLONE
153	-----	-----TXX-----		CARD4-Z CLONE
561	-----	-----TXX-----		CARD4L

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-----KKPKKKW-----				Majority
	650	660	670	680
133	-----SSPSMAW-----			CARD4-Y CLONE
133	-----SSPSMAW-----			CARD4-Z CLONE
641	IEFNQVQAMPTFTWMLRCITETQSQKVGQLAARGICANYL			CARDAL
-----KKCKXX-----				Majority
	690	700	710	720
142	-----TSCTRT-----			CARD4-Y CLONE
133	-----TSCTRT-----			CARD4-Z CLONE
651	KLTVCNAKGSADCSALSFLVLRHFPKRLALDLDNNNLNDYGV			CARDAL
-----				Majority
	730	740	750	760
148	-----			CARD4-Y CLONE
133	-----			CARD4-Z CLONE
711	RELQPCPSRLTVLRLSNQTDDGVKVLSEELTKYKINTY			CARDAL
-----ECK-----				Majority
	770	780	790	800
148	-----			CARD4-Y CLONE
133	-----			CARD4-Z CLONE
761	LGLYNNQITDVGARYTKILD ECKGLTHLSLYNNQITDVG			CARDAL
-----WXXXXXXXXX-----				Majority
	810	820	830	840
148	-----			CARD4-Y CLONE
133	-----			CARD4-Z CLONE
801	ARLGKNKITSEGGKYLALAVKNSKKSISEVGMWGNQVGDEG			CARDAL
XXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX				Majority
	850	860	870	880
149	-----			CARD4-Y CLONE
155	-----LRKQA-----			CARD4-Z CLONE
841	AKAFAEAIPNHPSLTTLSLASNGISTEGGKSLARALQQNT			CARDAL
XX				Majority
	890	900	910	920
149	-----			CARD4-Y CLONE
151	---QVL-----			CARD4-Z CLONE
851	SLEITWLCQNEELNDEVAESLAEMLKVNQTLKHLWLIQNQI			CARDAL
XX				Majority
	930	940	950	960
149	-----			CARD4-Y CLONE
154	-----			CARD4-Z CLONE
921	TAKSTAGLADALQSNTEITETICLNGWLIKPEAKVYEDEK			CARDAL

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<u>XXXXF</u>					Majority
149					
154	-	-	-	F	CRD4-Y CLONE
161	F	-	-	F	CRD4-Z CLONE
					CRD4L

Decorations: Decorations 11: Shade (with solid black) residues that match the Consensus exactly.

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CCACGCGTCCGCGGACCCGCGAGCGGTAGCGCCCTCCCTCCCAGCTGTTGTCCGCGCCGAT
CCGCGACCCCTAGTCCCCGATCCGCTTCTGAGAGTCACCGTACTCCAGGGCCAACTGAG
CCAAAGTCCTGCCAACTTGGGTGAGCAATGAAAGGCAGGATCCTGGGTGGTGGCCCTGAA
TCCTGATTTGTCTGCCCTGCCAGCGAGACACATGTGGTCAAAGATGAATTTGAGAAAAGT
AGCTGCTGGCTACTTGAACAATGGAGGAACACGGCCATCATGAGATGGAAGGCACCCCAT
TGGGTGTGCACTCCACATTAAGTCTGTAAGATCAACAGGGAAACATCTGGTCACCAACA
TTCGGAACACTCAGTGTCTGGTGGACAACCTTGTCTGGAGAATGGCTACTTCTCAGCCGAAG
ATGCAGAGATTGTGTGTGCTTCTCCCAACCAAGCCTGACAAGGTCCGAAAGATCCTTGACC
TGGTGCAGAGCAAAGGCGAGGAGGTGTCTGAGTTCTTCTCTACGTGCTGCAGCAGCTGG
AGGATGCTTACGTGGACCTCAGGCTGTGGCTCTCAGAAATTGGCTTCTCCCTTCCCAGC
TCATTCCGACCAAACTATCTCAATACTGACCCAGTAAGCAGGTATACCCAACAGCTGC
CACACCAACTGGGCGCGACTCCAAGTTCATGCTGTGCTACGCCCAGAAGGAGGACCTGC
TGCTGGAGGAGACCTATATGGACACACTCATGGGGCTSGTAGGCTTCAACAATGAAAACC
TGGGCAGCCCTAGGAGGCCTGATTGCTTCTGGACCACAGTACGGGCGTCTCTAACGAGC
ATGGCGAGACTGTCTTCTGTGTTCGGGGACGCGGAGTGGGCAAGTCCATGCTGCTGCAGA
GGTTGCAGAGCCTCTGGGCGTCAGGCAGGTTGACCTCCACAGCCAAATTCTTCTTCCACT
TCCGCTGCCGATGTTTCTGCTGCTTCAAGGAGAGCGACATGCTGAGTCTGCAGGACCTGC
TCTTCAAGCATTCTGCTACCCGAGCAGGACCCCGAGGAGGTGTTCTCCTTCTTGTCTGC
GCTTTCCCACACAGCGCTCTTCACTTTTGACGGCCTGGATGAGCTGCACTCAGACTTCG
ACCTGAGCCGCGTGGCGGATAGCTGCTGCCCCCTGGGAGCCGGCTCACCCCTCTGGTCTCTGC
TGGCTAACCTCCTAAGTGGGAGGCTGCTCAAGGGTGGCGGCAAATTGCTCACTGCTCSCA
CAGGCGTGGAGGTCCCCCGCCAGCTCCTGCGCAAAAAGGTGCTGCTCCGGGGCTTCTCCC
CAAGTCACCTGCGCGCTATGCCCCCGGATGTTCCCCGAGCGCACAGCGCAGGAGCATC
TGCTGCAGCAGCTGGATGCCAACCCCAACCTCTGCAGCCTGTGCGGGGTGCCGCTCTTCT
GTTGGATCATCTTCCGTTGTTTCCAGCACTTCCAGACGGTCTTCGAGGGCTCCTCTTCAC
AGTTGCCGGACTGTGCTGTGACCCTGACCGATGTCTTTCTGCTGGTCACTGAGGTGCATC
TGAACAGGCCGCGAGCCGAGCAGCCTGGTGCAGCGCAACACGCGCAGCCCGGGCGAAACCC
TACGTGCAGGCTGGCGCACGCTGCATGCGCTGGGAGAGGTGGCTCACCGAGGCACCCACA
AGAGCCTCTTTGTGTTTGGCCAGGAGGAGGTGCAGGCGTCAAGCTGCAGGAAGGAGATC
TGCAGCTGGGCTTCTGCGGGCTTTGCCCGATGTGGGCGCTGAGCAGGGCCAGTCTTACG
AATTTTCCACCTTACGCTCCAGGCCTTCTTCAACGCGCTTCTTCTCTGGTAGCAGATGACA
AAGTGAGCACCCGGGAGTTGCTGAGGTTCTTTCGAGAATGGACGTCTCTGAGAGGCAA

FIG. 15 (Page 1 of 3)

00720721 120100

CAAGCTCGTCCTGCCATTCTTCTTCTTCTCTCTTCCAGTGCCTGGGCGGCAGAAGCCGGT
TGGGCCCTGATCCTTTTCAGGAACAAAGATCACTTCCAGTTCCACCAACCTCTTCGTGTGCG
GGCTACTGGCCAAAGCCCTACAGAACTCCTTCGGCAGCTGGTGGCCCAAGGCTATCCTGA
GGAGGAAGCGCAAGGCCCTGTGGGCTCACCTGTTTGCTAGCCTGCGCTCCTACTTGAAGA
GCCTACCTCGGGTCCAGTCTGGAGGCTTTAACCAGGTGCATGCCATGCCACATTCTGT
GGATGCTGCGCTGCATCTATGAGACGCAGAGCCAGAAGGTGGGGCGCCTCGCCGCCAGGG
GCATCAGTGGGACTACCTCAAGCTGGCCTTTTGCAACGCTTGCTCTGCGGACTGCAGCG
CCCTGTCTTCTGCTCCTGCATCACTTCCACAGGCAGCTGGCCCTAGACCTGGACAACAACA
ACCTCAATGACTATGGCGTGCAGGAGCTGCAGCCTTGCTTTAGCCGTCTCACGGTTATCA
GACTCAGCGTCAACCAGATCACCGACACGGGGGTGAAGGTGCTATGTGAGGAACGACCA
AGTATAAGATCGTGACGTTCTGGGTTTATACAACAACCAGATAACTGATATCGGAGCCA
GGTATGTGGCCCAATCCTGATGAATGCAGAGGCCTCAAGCACCTTAAACTAGGGAAAA
ACAGAATAACAAGTGAGGGCGGGAAGTGTGTGGCTTTGGCTGTGAAGAACAGCACCTCCA
TCGTTGATGTTGGGATGTGGGGTAATCAGATTGGAGACGAAGGGGCAAAGGCCTTCGCAG
AGGCATTGAAGGACCACCCAGCCTGACCACTCTCAGTCTTGCAATCAATGGCATCTCTC
CGGAGGGAGGGAAGAGCCTTGGCGAGGCCCTGAAGCAGAACACCACACTGACAGTAATCT
GGCTGACCAAAAATGAACTTAATGATGAGTCTGCAGAGTGCTTCGCTGAGATGCTGAGAG
TGAACCAGACGCTACGGCATTTATGGCTGATCCAGAATCGCATCACAGCCAAGGGGACAG
CGCAGCTGGCGAGGGCACTGCAGAAGAACACAGCCATAACAGAGATTTGTCTCAATGGAA
ACTTGATTAAGCCCCAGGAGGCCAAAGTCTTCGAGAATGAGAAGAGAATCATCTGCTTCT
GACGGACGCTCCTGGGCAGGATCTTTGTCCTAGGTTGCTCCTCAGTCACAGACAGCACTG
TGCAGTCAGCAGGGTAGCAGGATGCTGTGCAGCGCCTGCAGCAAGGTGCCTGTGAGGAGC
CCACACCTCCACAGTGCACACCGATGTCCCTGCTCATGCTTGGACTGGTAGCACCCGCG
CCGCGGCTGAGACCTGCAGACGCAGGGAGTCTTAGGAACCATCGTCAACCACTCAAAGCC
AGCAGGGCATCTTCTGTACAAAGATCTCCCTGCATATCCACTAGACGGAAGCTGAAGGAA
CGCAACAGCAGAGGAGGCCAACAGACGCCTGGCTGAAGGCTCCGTGGGACCAACGGTGTG
ACCTTCAGAAAAGAGCTGGGAACCTTGAGCAGAGCCGATGGTAACCTTCTGGGGAAAGAAG
GCACCCAGTGACTGCATGGTTATTCTGAGTCCTCCTTCTGCTTAGTCCCTCTCACTG
TACAGGTCTGTTTCTTCTCGCAGCTGTGGCTGCTGAAGTAGGTCCACTGTGGGGAGAGC
TCATCACAGACTTTGGTTTCGGTTCTGGATTCTCAGTGGTGGCAACCGAGAGTCAGACGAT
ACCCTCTAGGTGAGTCTCAGAGGATCTCTATGCTGTGAGAGGGTTGAGGGCCCCACCCAGA
ATTTTTTTTTTTTACCAGTTTTTACTGTGCCTGCCCCAGGAGGGAGAATTACTTCCCAGC

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CTCCACAGCAGCAGGCATGGCTTGCCTCAATGGTCCTCAGATCCCAACAAACTCTCTCC
CTTGCCTGTGAGCAGAAAGTATCTTCATGTCTCAGAAGTTGGAGGGTGACTGGACACAG
TTAAGACTCAGAGAGCCAGCTGATAGCTCAAAGCAAAGCATGGCACATACCCACCACCAT
ACCATGGTGCAGCATGGGATGGGACASTTGGAAATGTTGCAGATAACGTGTTCTTTTGGCAG
TTCATTTGTTAATAAAATATTTAAAACGTTAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCG
G (SEQ ID NO:42)

FIG. 15 (Page 3 of 3)

00720724.120400

MEENGHHEMEGTPLGCHSHIKLLKINREHLVTNIRNTQCLVDNLLNGYFSAEDAEIVCA
OPTKPKVRKILDLVQSKGEEVSEFFLYVLQOLEDAYVDLRLNLSEIGFSPSQLIRTKTI
VNTDFVSRYTQQLRHQLGRDSKFMLCYAQKEDLLLEETYMDTLMGLVGFNNENLGSLGGL
DCLLDHSTGVLNEHGETVVFVGDAVGKSMMLQRLQSLWASGRLTSTAKFFFHFRCRMFS
CFKESDMLSLODLLFKHFCYPEQDPPEEVFSFLLRFPHTALFTFDGLDELHSDFDLSRVPD
SCCFWEPAPLPLVLLANLLSGRLLKGAGKLLTARTGVEVPRQLLRKKVLLRGFSPSHLRAY
ARRMFPERTAQEHLLOQLDANPNLCSLCGVPLFCWIIIFRCFQHFQTVFEGSSSQLPDCAV
TLTDVFLLVTEVHLNRPQPSSLVQRNTRSPAETLRAGWRTLHALGEVAHRGTDKSLFVFG
QEEVQASKLQEGDLQLGFLRALPDVGPEQGQSYEFFHLLTLOAFTAFFLVADDKVSTREL
LRFFREWTSPGEATSSSSCHSSFFSFQCLGGRSRLGPDPPFRNKDHFQFTNLFVCGLLAKAR
QKLLRQLVPKAILRRKRKALWAHLFASLSYLKSLPRVQSGGFNQVHAMPTFLWMLRCIY
ETQSQKVGRILAARGISADYLKLAFCNACSDCSALSFVLHHFHRQLALDLENNNLNDYGV
QELQPCFSRLTVIRLSVNQITDTGVKVLCEELTKYKIVTFLGLYNNQITDIGARYVAQIL
DECRGLKHLKLGKNRITSEGGKCVALAVKNSTSIVDVGWGNQIGDEGAKAFAEALKDHP
SLTTLSLAFNGISPEGGKSLAQALKQNTTTLTVIWLTKNELNDESAECFAEMLRVNQTLRH
LWLIQNRITAKGTAQLARALQKNTAITEICLNGNLIKPEEAKVFENEKRIICF
(SEQ ID NO:43)

FIG. 16

[illegible]

FIGURE 17

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FIG. 18 (1 of 10)

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 222. **Keywords**
 223. **Subject Headings**
 224. **Classification**
 225. **Indexing**
 226. **Keywords**
 227. **Subject Headings**
 228. **Classification**
 229. **Indexing**
 230. **Keywords**
 231. **Subject Headings**
 232. **Classification**
 233. **Indexing**
 234. **Keywords**
 235. **Subject Headings**
 236. **Classification**
 237. **Indexing**
 238. **Keywords**
 239. **Subject Headings**
 240. **Classification**
 241. **Indexing**
 242. **Keywords**
 243. **Subject Headings**
 244. **Classification**
 245. **Indexing**
 246. **Keywords**
 247. **Subject Headings**
 248. **Classification**
 249. **Indexing**
 250. **Keywords**
 251. **Subject Headings**

FIG. 18 (2 of 10)

ctgtcacaccagtggtcagagtgttaataattgcatggggacatgggggtgcaggggggtcgaaggct
gccctagcctgggaattggaaaacctggagtcctgttctctgtactctcagccagtgactctccct
ctgtagccccaggcagtcctcacactcagtgccaccctctgtccatctttttttttctccccaa
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caccatgtccggctaagttttttgtatttttagtaggacgggggtttccccatgttggccaggctg
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[illegible]

FIG. 18 (4 of 10)

cgatgggggttttctagataaacaatcatgtcgtctgcaaacagggacaatttgacttccctctttt
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 gtttttggccattcagratgatattggctgtgggtttgtcatagatagctcttattattttgaaa
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 aatagtttcagaaggaatgggtaccagttccctcttgtacctctggtagaattcggctgtgaatcc
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09728721.120400

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FIG. 18 (6 of 10)

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FIG. 18 (9 of 10)

[illegible]

[illegible]

FIG. 19

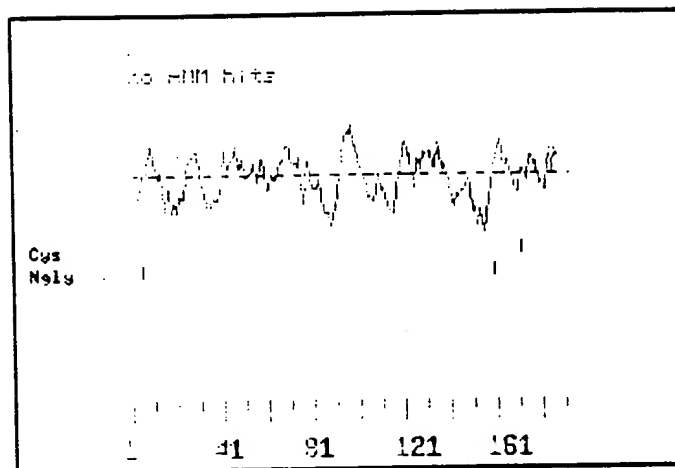


FIG 20

1► M G

3 ▶ R A R D A I L D A L E N L T A E E L K K

23 ▶ F K L K L L S V P L R E G Y G R I P R G

43 ▶ A L L S M D A L D L T D K L V S F Y L E

63 ▶ T Y G A E L T A N V L R D M G L Q E M A

83 ▶ G Q L Q A A T H Q G S G A A P A G I Q A

103 P P Q S A A K P G L H F I D Q H R A A

123▶ I A R V T N V E W L L D A L Y G K V L

143 ▶ D E Q Y Q A V R A E P T N P S K M R K

163 ▶ F S F T P A W N W T C K D L L L Q A L

183 ▶ E S Q S Y L V E D L E R S

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TATGCTTTTCGGTCGAACTT

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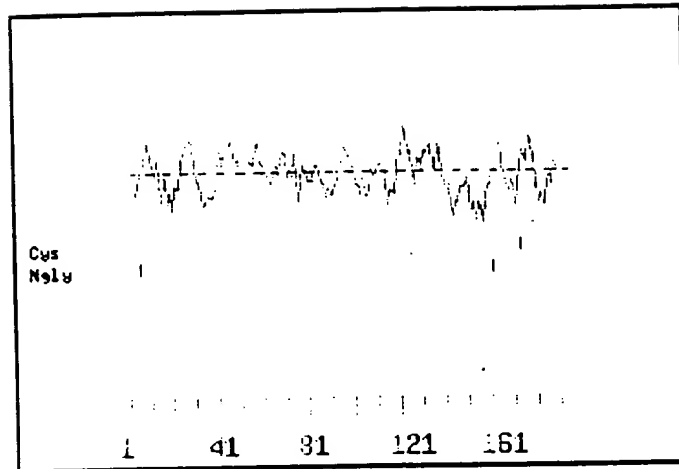


FIG. 22

1. The first part of the document is a list of references. The references are listed in a standard format, with the author's name, the title of the work, and the publisher. The references are as follows:

1. The first part of the document is a list of references. The references are listed in a standard format, with the author's name, the title of the work, and the publisher. The references are as follows:

68.2% identity; Global alignment score: 2377

FIG. 23 (1 OF 2)

FIG 23 (2 of 2)

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ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
 > hCARD5-protein 195 aa vs.
 > mCARD5-protein 193 aa
 scoring matrix: paml20.mat, gap penalties: -12/-4
 71.8% identity; Global alignment score: 712

```

      10      20      30      40      50      60
inputs MGRARDAILDALENLTAEELKKFKLKLSSVPLREGYGRIPRGALLSMDALDLTKLVSFY
      .....
      MGRARDAILDALENLSGDELKKFKMKLLTVOLREGYGRIPRGALLQMDAIDLTKLVSYY
      10      20      30      40      50      60

      70      80      90     100     110     120
inputs LETYGAELTANVLRDMGLQEMAGQLQAATHQGSGAAPAGIQAPPQSAAKPGLHFIDQHRA
      .....
      LESYGLELTMTVLRDMGLQELAEQLQT-TKEESGAVAAAASVPAQSTARTG-HFVDQHRQ
      70      80      90     100     110

      130     140     150     160     170     180
inputs ALIARVTNVEWLLDALYGKVLTDQYQAVRAEPTNPSKMRKLFSFTPAWNWTCKDLLLQA
      .....
      ALIARVTEVDGVLDALHGSVLTEGQYQAVRAETTSQDKMRKLFSFVPSWNLTKDSLLQA
      120     130     140     150     160     170

      190
inputs LRESQSYLVEDLERS
      .....
      LKEIHPYLVMDLEQS
      180     190

```

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1 CCCGCGTCCGGACTTCCCTTCCAGTGTGTTGTTCTCTCTGCTCTCTCCAACAGAAGGTATTTTIG
GGGCGCAGGCCTGAAGGGAAGGTACAAACAAGGAGAGACGAGAGAGGTTGTCTTCCATAAAAAAC

66 GCATGTTTTATCTTTGCTAAGTAGGATTTCTGTCTTTCTTTGTTAACACAGATTTCTTTCTGTGC
CGTACAAAATAGAAACGATTTCCTTAAAGACAGAAAGAAACAATTGTGTCTAAAGAAAGACACG

131 CAGAATGACCTGATCCATTTCTGGTTTGTAGAAAGCCATGGCTTCAGAGGGTGCTTCTCTCAGAA
GTCTTACTGGACTAGGTAAAGGACCAAACATCTTTCCGGTACCGAAGTCTCCCACGAAGGAGTCTT
----- 1 M A S E G A S S E -----

196 ATCATAGAAAAACAGCGAACAAAGTTGCTCAGTGTCTCTCCAACAAGATCCCGACTCTATCTTGA
TAGTATCTTTTGTGCTTGTTCACGAGTACACGAGGTTGTTCTAGGGCTGAGATAGAACCT
----- 10 I I E K Q R T K L L S V L Q Q D P D S I L D -----

261 CACGTTAACCTCTCGGAGACTGATTTCTGAGGAGGAGTATGAGACTCTAGAGGCAATTACAGATC
GTGCAATTGGAGAGCCTCTGACTAAAGACTCTCTCTCATACTCTGAGATCTCCGTTAATGTCTAG
----- 31 T L T S R R L I S E E Y E T L E A I T D -----

326 CTCTGAAGAAAAGCCGAAGCTGTTAATTTTGATCCAGAAGAAGGGAGAGGACAGCTGTTGTGT
GAGACTTCTTTTCGGCCTTCGACAATTAAACTAGGTCTTCTTCCCTCTCTGTGCAACAACA
----- 53 P L K K S R K L L I L I Q K K G E D S C C C -----

391 TTCCTCAAGTGTCTGTCTAATGCCCTTTCCACAGTCAGCTTCCACCTTGGGTTTAAAGCAGGAAGT
AAGGAGTTCACAGACAGATTACGGAAGGTGTGAGTCGAAGGTGGAACCCAAATTTCTGCTCTCA
----- 75 F L K C L S N A F P Q S A S T L G L K Q E V -----

456 TCCACGGCAGGGGACTGGAGAGGTTGTGAGGTGAGCAGGGGTTTGAAGATCCCTTTTCTCTTG
AGGTGCCGTCCCCTGACCTCTCCAACAGCTCCACTCGTCCCCAAACCTTCTAGGGAAAAGAGAAC
----- 96 P R Q G T G E V V E V S R G L E D P F S L -----

521 GGACCATAACCCAGAAATAGCAGAGCTCTCAGAAGAGAAAGAATGCCCGGGTCTGGGAGCTCCG
CCTGGTATTTGGGGTCTTTATCGTCTCGAGAGTCTTCTCTTTCTTACGGGCCCAGACCCTCGAGGC
----- 118 G T I T P E I A E L S E E K E C P G L G A P -----

586 GAGTTCTTCACCTGCAAGGAAAGCAGCCACAGGGAACCGGAAGTACCTTCTTGGGAGAATCAGGA
CTCAAGAAAGTGACGTTCCCTTTCTGTCGGTGTCCCTTGGCCTTCATGGAAGAACCCTCTTAGTCCT
----- 140 E F F T C K E S S H R E P E V P S W E N Q E -----

651 AGGGCGTGGTGCACAGCAAGTCACCGCTCCGCGTTCAGTCAAAGGAGTTGAGTATGAAGTTCCAG
TCCCGCACCACTGTGCTTCAAGTGGCGAGGCGCAAGTCAGTTTCTCAACTCATACTTCAAGGTC
----- 161 G R G A Q Q V T A P R S V K G V E Y E V P -----

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716 CAAGTATCTCCCTCTTAAGCGACGGGCGAGAGATACGAGGAGCCAGATGATTCCGCTGTACTTAGAA
 GTTCATAGAGGGAGAATTTCGCTGCCCGTCTCTATGCTCCTCGGTCTACTAAGCGACATGAATCTT
 183▶ A S I S L L S D G Q R Y E E P D D S L Y L E

781 GAAGGGGAAGGTGAAGAGTCTCTTGGGTACCCCTGAAGATGTTTTGGAGGAAGGGGCCGGCGATGA
 CTTCCCTTCCACTTCTCAGAGAACCCATGGGACTTCTACAAAACCTCCTTCCCGGCCGCTACT
 205▶ E G E G E E S L G Y P E D V L E E G A G D D

846 CCCACAGTGCCTTTGTATATGATAGTGAGGAGGAATGCGAGTATGAGGAAAACATGGGCTCCTCCG
 GGGTGTACGAAACATATACTATCACTCCTCCTTACGCTCATACTCCTTTTGTACCCGAGGAGGC
 226▶ P Q C F V Y D S E E E C E Y E E N M G S S

911 GTGAAGACAGTAGCTGCGACGACACTTCAGAGACCTGCGTTCCATTGGAAGGGGAGAAAAGCGT
 CACTTCTGTATCGACGCTGCTGTGAAGTCTCTGGACGCAAGGTAACCTTCCCTCTTTTCGCGA
 248▶ G E D S S C D D T S E T C V P L E G E K S A

976 GAAGAAAGAAAAAGAGTGTTCACACGCTCCTGTCTGTTTGAACATGGATAGAAACAGAAAGCT
 CTCTTTCTTTTCTCACAAGTTGTGCAGGACAGGACAAACTGTACCTATCTTTGTCTTTTGA
 270▶ E E R K R V F Q H V L S C L N M D R N R K L

1041 TCTCCCAGAGTTCGTGAGGCAGTTTTCCATAGACCGAGGATGTGAGTGGACACCCAAGACCCAG
 AGAGGGTCTCAAGCACTCCGTCAAAAGGTATCTGGCTCCTACACTCACCTGTGGGTCTTGGGGTC
 291▶ L P E F V R Q F S I D R G C E W T P K T P

1106 GAGACTTAGCTTGGAAATTTCTTGATGAAAGTTTCAGGCTTTAGACTCGACAGCCAGAGATTCTATC
 CTCTGAATCGAACCTTAAAGAACTACTTTCAAGTCCGAAATCTGAGCTGTCCGTCTCTAAGATAG
 313▶ G D L A W N F L M K V Q A L D S T A R D S I

1171 CTGAGGCCCGAGGTGGCGGGTGAAGAGAATGAAGAATTGCCGGCTGGAATAGAGAAGTTAGGCAT
 GACTCCGGGCTCCACCGCCCACTTCTCTTACTTCTTAACGGCCGACCTTATCTCTTCAATCCGTA
 335▶ L R P E V A G E E N E E L P A G I E K L G I

1236 TGGAGACCCCCAAACCATCCATCCCTGGATGTCTCTGCGCCTGCATGCTTTTGTGCAGACAGCT
 ACCTCTGGGGGTTTGGTAGGTAGGGGACCTACAGGAGACGCGGACGTACGAAACAGCTCTGTGCA
 356▶ G D P Q T I H P L D V L C A C M L C A D S

1301 CCTTGACGCGTGAAGTCATGTCAAACATGTACCAATGCCAGTTTGCTCTTCCCTGCTACTGCCA
 GGAACGTCGCACCTCAGTACAGTTTGTACATGGTTACGGTCAAACGAGAAGGGGACGATGACGGT
 378▶ S L Q R E V M S N M Y Q C Q F A L P L L L L P

1366 GATGCTGAGAACAAACAAAACCTCTTAATGGTAGGGCCATGAAGGACTTAAAGCAGCCCTCAGC
 CTACGACTCTTGTGTGTTTTGGAGAATTACCATCCCCGCTACTTCTGAATTTCTGTCGGGAGTGC
 400▶ D A E N N K N L L M V G A M K D L K Q P S A

FIG. 25 (3 of 7)

2796 GCCTTCTCAGCAGAGACCCAGTCAGCCTAAATCATTCAGACCAAGCCTTCACAGGCCAGGGCCT
CGGAAGAGTCGTCCTCTGGGTCACTCGGATTTAGTAAGGTCTGGTTCGGAAGTGTCGGTCCCGGA
876▶ P S Q Q R P S Q P K S F Q T K P S Q A R A

2861 GCCACCCAAGAGCAGGGAGACGTTAAAGAACATACTCTGGAGATCTGGGAAATAAAGTATGGGCT
CGGTGGGTTCCTCGTCCCTCTGCAATTTCTTGATGAGACCTCTAGACCCCTTTATTTTCATACCCGA
898 C H P R A G R R

2926 TTGCTTAAGTATTCTTTTTTCATATAGCAAGCTGAAGAAAAGTTTTAGTGAAAGACTGATAAAAAGT
AACGAATTCATAAGAAAAAGTATATCGTTCCACTTCTTTTTCAAAATCACTTTCTGACTATTTTCA

2991 AGCAAAACCCAAAAAGGTATGCAAAGTCTTAAGTGCATAGCAAAGTATCCAAGTGTGGGAAATA
TCGTTTTGGGTTTTTTCCATACGTTTCAGAAATTCACGTATCGTTTTCATAGGTTACACCCCTTTAT

3056 TGGAAAGCAGTTAAAAGTAGAATCTGGCTGGGCA TGGTGGCACACATCTACAGGTTTTAGCATGGG
ACCTTCGTCAATTTTCATCTTAGACCCGACCCGTACCACCGTGTGTAGATGTCCCAAATCGTACCC

3121 AGGGCTCTGTCTATCCCACTCAGAGAAGCAGGCAGATCTCTGTGTGTTTTGAGGCCAGTCTGGTCT
TCCCGAGACAGTAGGGTTGAGTCTCTTCGTCCGTCTAGAGACACACAAACTCCGGTCAGACCCAGA

3186 ACATAACAACGACACAAGCAAGTCTTACATCAGCCATACTACAAAATGAGACCCCATCTGGGGAC
TGTATTGTTGCTGTGTTTCGTTTCAGGATGTAGTCGGTATGATGTTTTACTCTGGGGTAGACCCCTG

3251 AAAAGGGTTGGATCTAACATCAAACCAAAGAAATCAGTCAAGTATTCCAGAAGGCATCATTAAAT
TTTTCCCAACCTAGATTGTAGTTTGGTTTCTTTAGTCAGTTCATAAGGTCTTCCGTAGTAATTAA

3316 ACACTCAGTGGGTACCACAACCAAACCATCTCGACAACCTAACCCCTTAAAGGAGCAAGAAGGA
TGTGAGTCACCCCAATGGTGTGGTTTCGTATGAGCTGTTGATTGGGGGATTTCTCTGTTCTTCTCT

3381 GTTGGGTGGGTGTTAGGCTGAACATGATTGGGGAAGAACTGAAGATAGATAAGGTCATTTCGTAAT
CAACCCACCCACAATCCGACTTGTACTAACCCTTCTTGACTTCTATCTATTCCAGTAAGCATTAA

3446 ACAGGTTATGGGACTTGTCAAATCCATTAAATGCAATATTAAGAAGCAGTGGGAATCTTAAGGCT
TGTCCAAATACCCCTGAACAGTTTAGGTAATTTACGTTATAATTTCTTCGTACCCCTTAGAATTCGGA

3511 ACATTAAAGCTCCAGTGAAGTCCCAACCCCTCCCTTATTAGATGATGTGAGATTTGAACCCCAAGTGAA
TGTAATTCGAGGTCACTCAGCGTTGGGAGGGGATAATCTACTACACTCTAAACTTTGGGGTCACTT

3576 TGGGGTGTGTCTGATAGCCCGTGTGTGTGACAACTGTGTAATTATAAAGTGATGAAAACGTGGG
ACCCACACAGACTATCGGGCACACACTGTTTGACACATTAATATTTCACTACTTTTGCACCC

3641 AGTTCAGCTTATCTGTGTTGAAGAAAGGCTGCTTCAGAGGTGCCTTGGTTTTGGGTTTATGATCA
TCAAGTCGAATAGACACAACCTCTTTCGACGAAGTCTCCACGGAACCAAAACCAAACTACTAGT

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3706 GCCACTGAGCAGATACTCTGCACCATTGGTACAGTTAAATCAGCTTGCTTCTGGTAATAGCCCCA
CGGTGACTCGTCTATGAGACGTGGTAACCAATGTCAATTTAGTCCAACGAAGACCATTATCGGGGT

3771 ATCTACCACATTTATCCCTTACAGGCGGAAATAATGAATGATCAGCAAAACATCCAATTTTACCT
TAGATGGTGTAAATAGGGAATGTCCGCCCTTATTACTTACTAGTCGTTTGTAGGTTAAATGGA

3836 TAACCTTGGTACTGATTGTATATGTATCATTCTTTATATAATAGCTAAGAAAATTTAGCTCATT
ATTGGAACCATGACTAAACATATACATAGTAAGAAATATATTATCGATTCCTTTTAAATCGAGTAA

3901 AGGGGTCTGATATATTAGTTTAAATGGTTTGAAGTCAGAAATGTGTTAGTTTAAATTTTAGAGT
TCCCCAAGACTATATAATCAAATTACCAAACCTTCAGTCTTTACACAATCAAAAATTTAAATCTCA

3966 TAATTGAAAATATTGAGATGAATTTACAAAGGCTATAAGTAATGTTTGAGAGGGTTATAATTTT
ATTAACCTTTTATAACTCTACTTAAATGTTTCCGATATTCATTACAAACTCTCCCAATATTAAAAA

4031 GTAGACTCATACTGTTCTGAACATTTGGATAGCTTCTCGTAGTTAGCAGTGTTATAGAAGAATAT
CATCTGAGTATGACAAGACTTGTAAACCTATCGAAGAGCATCAATCGTCACAATATCTTCTTATA

4096 ATTTGATTTCAGGTATTTAACCAGAGCTGCTCTTAGTTTAAAGTGTACCAAGAGTCAATAAAAG
TAAACTAAGTCATAAAATGGTCTCGACGAGAATCAAAAATTCACAGTGGTTCTCAGTTATTTTC

4161 GCTACATTATCTGAACATGTGGGAACACAACCTGTGACCTTACACTTAAGAGACTGAGGAAGGGAA
CGATGTAATAGACTTGTACACCTTGTGTTGACACTGGAATGTGAATTCCTGACTCCTTCCCTT

4226 ATCAAGGTTCAAGCCAGCAGCACATAGTGAGACCAGGTCTCAAGACACAAAACTATCCACCTTA
TAGTTCCAAGTTCGGTCTGCTGTATCACTCTGGTCCAGAGTTCGTGTGTTTTGATAGGTGGAAT

4291 AGGAAGATTTTAAATTTGCCTCATTAAGAAATAAGTAAGATTTATAAATGGACTAAATGTCA
TCCTTCTAAAAATTTAAACGGAGTAATTCCTTTATTTTCAATCTAAATATTTAACCTGATTACAGT

4356 CATCTTTGAACTTATGACTGTTTAAATTTTGTGACTTAAAGTTTAAATTTTATTATTGTATGCGTGT
GTAGAAACTTGAATACTGACAAATTTAAAAAACTGAATTTCAAAATTAATAACATACGCACA

4421 GTTGTATGTGTGTCACATGTGTGCCACTGCATGTATGTGGAGGCCATCAGACAATGTTGTAGAG
CAACATACACACAGTGTACACACGGTGACGTACATACACCTCCGGTAGTCTGTTACAACATCTC

4486 TCTGTTCTTTCTCTTAGCCCTATGTGTTTTACCCACTGAGCTAGGCCACCTACTCCTATAAGTC
AGACAAGAAAGGAGAATCGGGATACACAAAATGGGTGACTCGATCCGGTGGATGAGGATATTTCAG

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4551 TAATTTTAAATAGTAAATAGTTCTAAGAAGTCAATCAGGGAAAAAATGGCTGTCAAAGTCTCA
ATTAAAAATTATCATTTTATCAAGATTCTTCAGTTAGTCCCTTTTTTTACCGACAGTTTCAGAGT

4616 AAGAAAAATCGTATTAGCCATGGATAGAGACTCACCTCTTGAAATCATTTGTGTCTGAGAATAGCC
TTCTTTTTAGCATAATCGGTACCTATCTCTGAGTGGAGAACTTAGTAAACACAGACTCTTATCGG

4681 TAATATCACAATAATGTGTTTGTACATGTGTTAGTTAATATTGTTTTTCAGAGTATTTAATCTCTC
ATTATAGTGTATTACACAAACATGTACACAAATCAATTATAACAAAAGTCTCATAAATTAGAGAG

4746 ATGATTATTGTAAAGATGAAAAAGAAATAGTGGGCAATGTATGTGAGTATTTAATTTTCCTGA
TACTAATAACATTTCTACTTTTTCTTTATCACCCGTTACATACACTCATAAATTAAACGGACT

4811 CAATTCCTGTCTTTTAGAATGATAAATGTAAGAAGTAAAATAAAACGGTTTCATTCTCAGAACAACT
GTTAAGACAGAAAAATCTTACTATTTACATTTCTCATTTTATTTTGCCAAGTAAGAGTCTTGTGTA

4876 AAGCCAGCTCACTTAAGTCTGGGCCCTGCTGGCATTGGCTAGTCTAGCTACCCCCACCCAAACAC
TTCGGTCGAGTGAATTCAGACCCGGGACGACCGTAACCGATCAGATCGATGGGGGTGGGTTTGTG

4941 AAAAGTTTAGAGAAGAAAAATGACTGAGTCAAGCTTGCCTAATGACTTTTGGACATAAAGTTTATG
TTTTCAAATCTCTTCTTTTACTGACTCAGTTTGAACGGATTACTGAAAACCTGTATTTCAAATAC

5006 GTCCTAGAAAGCCTTAAAAATAAGTAGGATATAAAACATGTAAATTAACCCACACATTATGTGGGT
CAGGATCTTTCCGAATTTTATTCATCCTATATTTGTACATTTAATTGGGTGTGTAATACACCCA

5071 TGAGAAGCAGAAAAATGTCAGTAGAACACTCGGCCAGTGCATAAAGAAGGAAGAGACCTCTGTTT
ACTCTTCGTCTTTTACAGTCACTCTGTGAGCCGGTCACGTATTTCTTCTCTCTGGAGACAAG

5136 TGGGTTATAAAACTGCTCTTTGTGCTCAATTTGTCCCTGCTTTTGTGTTGCCAGAATGTACAAGA
ACCCAATATTTTGACGAGAAACACGAGTTAAACAGGGGACGAAAACAAACGGTCTTACATGTTCT

5201 TTATAAAATAAACTCACTTTTACTTTTTAAAAAAGGGCGG
AATAATTTTATTTGAGTGAAAAATGAAAAATTTTTTTTTTTTTTTTCCCGCC

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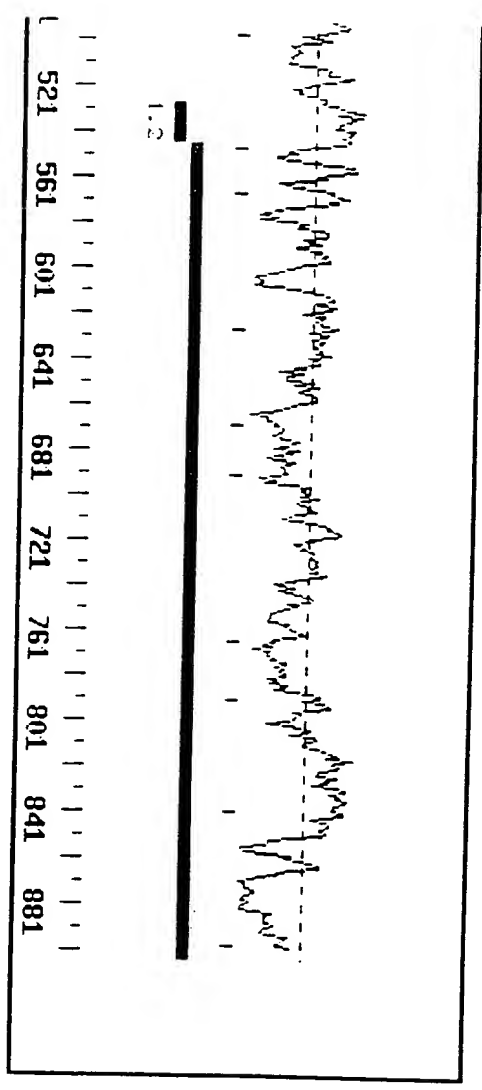
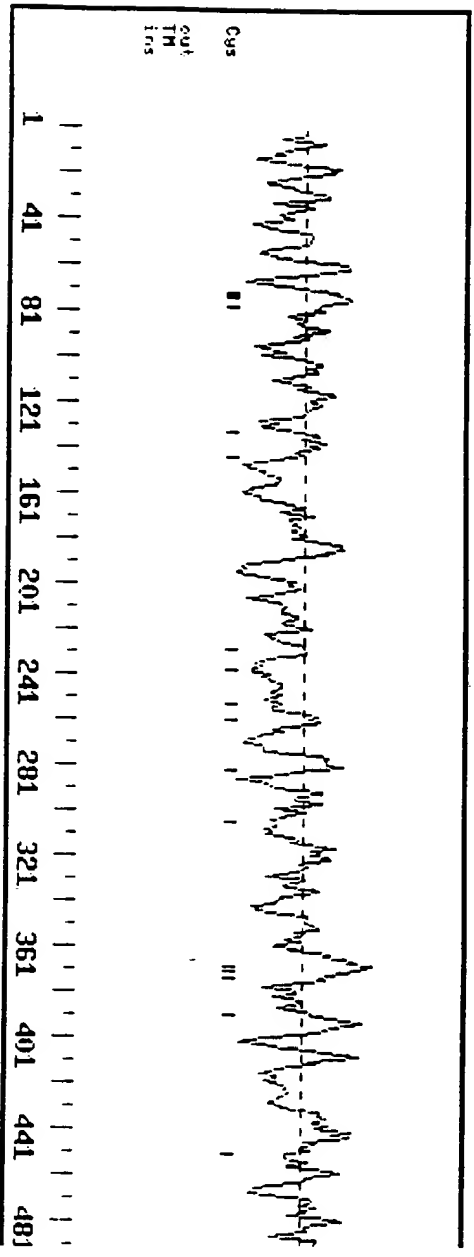


FIG. 26

09728721.120100

[illegible]

FIG 27

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CACGCGTCCGCCGGATCAGAGAGTGCTCCGAGCTGGGTGCCCACTGTGCTTGTATCTGCACTCTCCAACACTAGGC 79
 ATCATTGACATGTTAAAGCTTAGCCAAATAGAATTGTTCTTTGTCACTCTTTTAACTTTTACTTATTCATTAGGAT 158
 GATTTTCATAATATATTTCTGTTTGTAGAGGAAACAGGAACA ATG GCT ACC GAG AGT ACT CCC TCA GAG 226
 I I E R E R K K L L E I L Q H D P D S I 29
 ATC ATA GAA AGA GAA AGA AAA AAG TTG CTT GAA ATC CTT CAA CAT GAT CCT GAT TCT ATC 286
 L D T L T S R R L I S E E E Y E T L E N 49
 TTA GAC ACG TTA ACT TCT CGG AGG CTG ATT TCT GAG GAA GAG TAT GAG ACT CTG GAG AAT 346
 V T D L L K K S R K L L I L V Q K K G E 69
 GTT ACA GAT CTC CTG AAG AAA AGT CGG AAG CTG TTA ATT TTG GTA CAG AAA AAG GGA GAG 406
 A T C Q H F L K C L F S T F P Q L A A I 89
 GCG ACC TGT CAG CAT TTT CTC AAG TGT TTA TTT AGT ACT TTT CCA CAG TTA GCT GCC ATT 466
 C G L R H E V L K H E N T V P P Q S M G 109
 TGC GGC TTA AGG CAT GAA GTT TTA AAA CAT GAG AAT ACA GTA CCT CCT CAA TCT ATG GGG 526
 A S S N S E D A F S P G I K Q P E A P E 129
 GCA AGC AGT AAT TCA GAA GAT GCT TTT TCT CCT GGA ATA AAA CAG CCT GAA GCC CCT GAG 586
 I T V F F S E K E H L D L E T S E F F R 149
 ATC ACA GTG TTC TTC AGT GAG AAG GAA CAC TTG GAT TTG GAA ACC TCT GAG TTT TTC AGG 646
 D K K T S Y R E T A L S A R K N E K E Y 169
 GAC AAG AAA ACT AGT TAT AGG GAA ACA GCT TTG TCT GCC AGG AAG AAT GAG AAG GAA TAT 706
 D T P E V T L S Y S V E K V G C E V P A 189
 GAC ACA CCA GAA GTC ACA TTA TCA TAT TCA GTT GAG AAA GTT GGA TGT GAA GTT CCA GCA 766
 T I T Y I K D G Q R Y E E L D D S L Y L 209
 ACT ATT ACA TAT ATA AAA GAT GGA CAG AGA TAT GAG GAG CTA GAT GAT TCT TTA TAC TTA 826
 G K E E Y L G S V D T P E D A E A T V E 229
 GGA AAA GAG GAA TAT CTA GGA TCT GTT GAC ACC CCT GAA GAT GCA GAA GCC ACT GTG GAA 886
 E E V Y D D P E H V G Y D G E E D F E N 249
 GAG GAG GTT TAT GAT GAC CCA GAG CAC GTT GGA TAT GAT GGT GAA GAG GAC TTC GAG AAT 946
 S E T T E F S G E E P S Y E G S E T S L 269
 TCA GAA ACC ACA GAG TTC TCT GGT GAA GAA CCA AGT TAT GAG GGA TCA GAA ACC AGC CTT 1006
 S L E E E Q E K S I E E R K K V F K D V 289
 TCA TTG GAG GAG GAA CAG GAG AAA AGT ATA GAA GAA AGA AAA AAG GTG TTT AAA GAT GTC 1066
 L L C L N M D R S R K V L P D F V K Q F 309
 CTG TTA TGT TTG AAC ATG GAT AGA AGC AGA AAG GTT CTG CCA GAT TTT GTT AAA CAA TTC 1126
 S L D R G C K W T P E S P G D L A W N F 329
 TCC TTA GAT CGA GGA TGT AAG TGG ACC CCT GAG AGT CCA GGA GAC TTA GCC TGG AAT TTC 1186
 L M K V Q A R D V T A R D S I L S H K V 349
 CTG ATG AAA GTT CAA GCA CGA GAT GTG ACG GCT AGG GAT TCA ATC CTC AGT CAC AAG GTT 1246
 L D E D S K E D L L A G V E N L E I R D 369
 CTG GAT GAA GAT AGC AAG GAG GAT TTG CTG GCT GGA GTG GAG AAT TTG GAA ATT CGA GAC 1306

00720734 120400

FIG. 2B (1 of 4)

[illegible]

FIG. 28 (2 OF 4)

002031-102200

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P F Q N A G A Q G R G K S F G I Q S F H 789
CCT TTT CAG AAT GCA GGG GCC CAG GGC CGA GGT AAA AGT TTT GGT ATT CAA TCC TTC CAT 2566

P Q I F Y S G E R F M K F S R V A R G C 809
CCC CAG ATA TTT TAT TCA GGT GAA AGA TTC ATG AAA TTT TCC AGA GTT GCT CGG GGA TGT 2626

H S N G T F G R L P R P I C Q H V Q A C 829
CAC TCG AAT GGA ACA TTT GGG AGA CTG CCA AGA CCC ATT TGT CAG CAT GTA CAG GCC TGC 2686

P E R P Q M M G T L E R S R A V A S K I 849
CCT GAG AGA CCA CAA ATG ATG GGA ACT CTT GAA AGG TCT AGG GCA GTA GCC TCC AAG ATA 2746

G H S Y S L D S Q P A R A V G K P W P Q 869
GGT CAC TCC TAT TCC CTG GAT TCA CAG CCA GCA AGA GCA GTA GGG AAG CCA TGG CCT CAG 2806

Q A C T R V T E L T E A T G K L I R T S 889
CAA GCT TGC ACC AGG GTA ACA GAG TTA ACT GAA GCA ACT GGA AAA CTG ATA AGA ACA TCC 2866

H I G K P H P Q S F Q P A A A T Q K L R 909
CAT ATT GGA AAG CCT CAC CCT CAG TCC TTT CAA CCA GCA GCA GCC ACA CAA AAA CTA AGA 2926

P A S Q Q G V Q M K T Q G G A S N P A L 929
CCT GCT TCT CAG CAA GGA GTC CAG ATG AAG ACA CAA GGT GGG GCT TCA AAT CCA GCT CTC 2986

Q I G S H P M C K S S Q F K S D Q S N P 949
CAA ATA GGG TCC CAT CCC ATG TGC AAG AGC TCT CAG TTC AAA TCC GAT CAG TCC AAC CCA 3046

S T V K H S Q P K P F H S V P S Q P K S 969
TCC ACA GTC AAA CAC TCC CAG CCT AAA CCC TTC CAT TCT GTG CCC TCT CAA CCT AAA TCC 3106

S Q T K S C Q S Q P S Q T K P S P C K S 989
TCT CAG ACA AAA TCC TGT CAG TCC CAG CCC TCC CAA ACT AAA CCT TCT CCA TGC AAA TCT 3166

T Q P K P S Q P W P P Q S K P S Q P R P 1009
ACT CAG CCT AAG CCA AGC CAG CCC TGG CCT CCC CAG TCT AAG CCT TCT CAG CCC AGA CCC 3226

P Q P K S S S T N P S Q A K A H H S K A 1029
CCT CAA CCT AAG TCA TCC TCA ACC AAT CCT TCA CAA GCT AAG GCA CAC CAC TCA AAA GCA 3286

G Q K R G G K H * 1038
GGG CAG AAG AGG GGA GGG AAG CAT TAA 3313

AGAGCTAACTCCAGAGATCTATAAAGCATATCCTTTACCCAGGCCATTCTATCATATAGTAAGCAGAAGAGTTGCCAT 3392

GAAAGTAAAAGACTACTGTTCATTAGCATGTAAAACAAAGAAAGATATACATGACCGAATTGGATATCTTTGTTTGTGTTG 3471

TTTGAGACAGAGTTTCACTCTTGTGTGCCAGGCTGGAGTGCAATGGCAGATCTCGGCTCACCGCAACCTCTGCTTCCT 3550

GGCTTAAAGTGATTCTCTGCCTCAGCCTCTCGAGTAGCTGGGATTACAGGCATGCACCACCACACCCAGCTAATTTTG 3629

TATTTTTAGTAGAGGCAGGGTTTCTCCATGTTGGTCAGGCTGGTCTTGAACCTCCCGACCTCAGGTGATCCGCCCCACCTA 3708

GGCCTCTCAAAGTGTGGGATTACGTGTGTAAGCCACAGTCCCGAGCCGAATTGGATATCTTTAAGATATCTGTAAGT 3787

GTTATATCCCTAACCAAGAAGAAAAATATGAAAAATAATTAAGACTAGAAATCAAGCAGTAGATAATTGAATCCAATCTTG 3866

GGTATTATTAGATAATGTATAACTTGCACCCAGGGAATGGGGGTCTATGAGACAACCCCACTTGGAGAAGAATGGGGTT 3945

AGGGTCTCTAATTGCAAAGTGACTGTACAATAGGACGAAAGTTGCCTCTGTGTCTGAGAAAGTATCTTAGTTGTTGGCT 4024

GCTCCAGAGGTATCTTTGTCAAAAGCTTCTGGTTCAATATCAGCCACTGAGCAGATAACCCCTGCTTATTGGTGTTGGTT 4103

AAATCAACTAGCTTCTGCTAATAGCCCCAATTTGCTTGAATGGGAAAACCTCTCTCATTTGACCCTTATAGGTAGAAATA 4182

ATGAATTAAACAACCAATAAAATTAATCATTTGGCATTAAAAAAAAAAAAAAAAAAAAA 4244

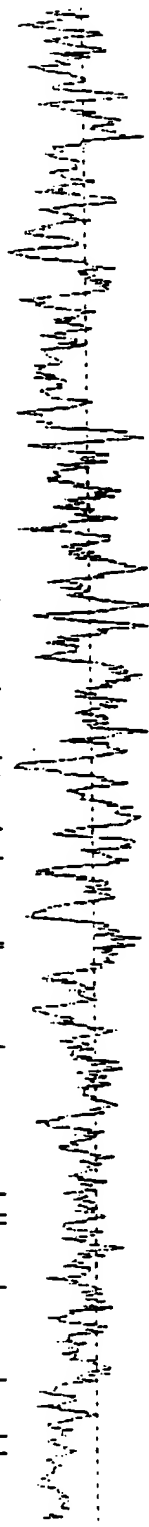
FIG. 28 (4 of 4)

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0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5
7.0
7.5
8.0
8.5
9.0
9.5
10.0

1 41 81 121 161 201 241 281 321 361 401 441 481 521 561 601 641 681 721 761 801 841 881 921 961 1001

0.5 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5 5.0 5.5 6.0 6.5 7.0 7.5 8.0 8.5 9.0 9.5 10.0



00728724.1E03100

FIG. 29

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00720721 120400

CONSENSUS *->maederrlLkknrvrliesLgldvLdelLdvLlekdvlnikeeEkik
 +++ + ** r++l+e+L+ d d +Ld L +++++ ++e E
CARD6 5 STP--SEIIERERKKLLEILQHD-PDSILDTLTSRRLISEEEYETLE 48

CONSENSUS ragakledDKarelvdslqrrgsqafdafidaledTgqsyLAdvLel<-*
 + l + r l++ +q++g. + ++ f+ +l++ LA++ +l
CARD6 49 NVTDLLKK--SRKLLILVQKKGEATCQHFLKCLFS-TFPQLAAICGL 92

DO NOT WRITE IN THESE SPACES

FIG. 31